



## SEQUENCE LISTING

### GENERAL INFORMATION:

(i) APPLICANTS:

Metz, James G.  
Lardizabal, Kathryn D.  
Lassner, Michael

(ii) TITLE OF INVENTION: Nucleic Acid Sequences Encoding in A  
Cytoplasmic Protein Involved in Fatty Acyl-CoA Metabolism

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Calgene, Inc.

(B) STREET: 1920 Fifth Street

(C) CITY: Davis

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 95616

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: Macintosh 7.0

(D) SOFTWARE: Microsoft Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/657,749

(B) FILING DATE: 30-MAY-96

(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/13686

(B) FILING DATE: 30-NOV-94

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/265,047

(B) FILING DATE: 23-JUN-94

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/160,602

(B) FILING DATE: 30-NOV-93

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/066,299

(B) FILING DATE: 20-MAY-93

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/09863

(B) FILING DATE: 13-NOV-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/933,411

(B) FILING DATE: 21-AUG-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/796,256

(B) FILING DATE: 20-NOV-91

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Elizabeth Lassen

(B) REGISTRATION NUMBER: 31,845

(A) NAME: Donna E. Scherer

(B) REGISTRATION NUMBER: 34,719

(A) NAME: Carl J. Schwedler

(B) REGISTRATION NUMBER: 36,924

(C) REFERENCE/DOCKET NUMBER: CGNE 101-2 WO

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (916) 753-6313

(B) TELEFAX: (916) 753-1510

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AAATCCTCCA CTCATACACT CCACTTCTCT CTCTCTCTCT CTCTCTCTGA AACAAATTTGA      60

GTAGCAAACCT TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT      112
      Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu
      1              5              10

GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA      160
Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys
      15              20              25

ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC      208
Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu
      30              35              40

TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG      256
Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
      45              50              55

CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT      304
Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
      60              65              70              75

TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA      352
Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
      80              85              90
```

CQC	GGT	GAT	ATT	ACT	GGT	GAA	GAC	TTG	TGT	CTC	AAA	GAC	GTC	AAT	TTG	400
Pro	Gly	Asp	Ile	Thr	Gly	Glu	Asp	Leu	Cys	Leu	Lys	Asp	Val	Asn	Leu	
			95					100					105			
AAG	GAA	GAA	ATG	TGG	AGG	GAA	ATC	GAT	GTT	GTT	GTC	AAT	CTA	GCT	GCT	448
Lys	Glu	Glu	Met	Trp	Arg	Glu	Ile	Asp	Val	Val	Val	Asn	Leu	Ala	Ala	
		110					115					120				
ACA	ATC	AAC	TTC	ATT	GAA	AGG	TAC	GAC	GTG	TCT	CTG	CTT	ATC	AAC	ACA	496
Thr	Ile	Asn	Phe	Ile	Glu	Arg	Tyr	Asp	Val	Ser	Leu	Leu	Ile	Asn	Thr	
		125				130					135					
TAT	GGA	GCC	AAG	TAT	GTT	TTG	GAC	TTC	GCG	AAG	AAG	TGC	AAC	AAA	TTA	544
Tyr	Gly	Ala	Lys	Tyr	Val	Leu	Asp	Phe	Ala	Lys	Lys	Cys	Asn	Lys	Leu	
140					145					150					155	
AAG	ATA	TTT	GTT	CAT	GTA	TCT	ACT	GCT	TAT	GTA	TCT	GGA	GAG	AAA	AAT	592
Lys	Ile	Phe	Val	His	Val	Ser	Thr	Ala	Tyr	Val	Ser	Gly	Glu	Lys	Asn	
				160					165						170	
GGG	TTA	ATA	CTG	GAG	AAG	CCT	TAT	TAT	ATG	GGC	GAG	TCA	CTT	AAT	GGA	640
Gly	Leu	Ile	Leu	Glu	Lys	Pro	Tyr	Tyr	Met	Gly	Glu	Ser	Leu	Asn	Gly	
			175					180					185			
AGA	TTA	GGT	CTG	GAC	ATT	AAT	GTA	GAG	AAG	AAA	CTT	GTG	GAG	GCA	AAA	688
Arg	Leu	Gly	Leu	Asp	Ile	Asn	Val	Glu	Lys	Lys	Leu	Val	Glu	Ala	Lys	
		190					195					200				
ATC	AAT	GAA	CTT	CAA	GCA	GCG	GGG	GCA	ACG	GAA	AAG	TCC	ATT	AAA	TCG	736
Ile	Asn	Glu	Leu	Gln	Ala	Ala	Gly	Ala	Thr	Glu	Lys	Ser	Ile	Lys	Ser	
	205					210					215					

ACA	ATG	AAG	GAC	ATG	GGC	ATC	GAG	AGG	GCA	AGA	CAC	TGG	GGA	TGG	CCA	784
Thr	Met	Lys	Asp	Met	Gly	Ile	Glu	Arg	Ala	Arg	His	Trp	Gly	Trp	Pro	
220					225				230						235	
AAT	GTG	TAT	GTA	TTC	ACC	AAG	GCA	TTA	GGG	GAG	ATG	CTT	TTG	ATG	CAA	832
Asn	Val	Tyr	Val	Phe	Thr	Lys	Ala	Leu	Gly	Glu	Met	Leu	Leu	Met	Gln	
				240					245					250		
TAC	AAA	GGG	GAC	ATT	CCG	CTT	ACT	ATT	ATT	CGT	CCC	ACC	ATC	ATC	ACC	880
Tyr	Lys	Gly	Asp	Ile	Pro	Leu	Thr	Ile	Ile	Arg	Pro	Thr	Ile	Ile	Thr	
			255					260					265			
AGC	ACT	TTT	AAA	GAG	CCC	TTT	CCT	GGT	TGG	GTT	GAA	GGT	GTC	AGG	ACC	928
Ser	Thr	Phe	Lys	Glu	Pro	Phe	Pro	Gly	Trp	Val	Glu	Gly	Val	Arg	Thr	
		270					275					280				
ATC	GAT	AAT	GTA	CCT	GTA	TAT	TAT	GGT	AAA	GGG	AGA	TTG	AGG	TGT	ATG	976
Ile	Asp	Asn	Val	Pro	Val	Tyr	Tyr	Gly	Lys	Gly	Arg	Leu	Arg	Cys	Met	
	285					290					295					
CTT	TGC	GGA	CCC	AGC	ACA	ATA	ATT	GAC	CTG	ATA	CCG	GCA	GAT	ATG	GTC	1024
Leu	Cys	Gly	Pro	Ser	Thr	Ile	Ile	Asp	Leu	Ile	Pro	Ala	Asp	Met	Val	
300					305					310					315	
GTG	AAT	GCA	ACG	ATA	GTA	GCC	ATG	GTG	GCG	CAC	GCA	AAC	CAA	AGA	TAC	1072
Val	Asn	Ala	Thr	Ile	Val	Ala	Met	Val	Ala	His	Ala	Asn	Gln	Arg	Tyr	
				320					325					330		
GTA	GAG	CCG	GTG	ACA	TAC	CAT	GTG	GGA	TCT	TCA	GCG	GCG	AAT	CCA	ATG	1120
Val	Glu	Pro	Val	Thr	Tyr	His	Val	Gly	Ser	Ser	Ala	Ala	Asn	Pro	Met	
			335					340					345			
AAA	CTG	AGT	GCA	TTA	CCA	GAG	ATG	GCA	CAC	CGT	TAC	TTC	ACC	AAG	AAT	1168
Lys	Leu	Ser	Ala	Leu	Pro	Glu	Met	Ala	His	Arg	Tyr	Phe	Thr	Lys	Asn	
		350					355					360				
CCA	TGG	ATC	AAC	CCG	GAT	CGC	AAC	CCA	GTA	CAT	GTG	GGT	CGG	GCT	ATG	1216
Pro	Trp	Ile	Asn	Pro	Asp	Arg	Asn	Pro	Val	His	Val	Gly	Arg	Ala	Met	
	365					370					375					
GTC	TTC	TCC	TCC	TTC	TCC	ACC	TTC	CAC	CTT	TAT	CTC	ACC	CTT	AAT	TTC	1264
Val	Phe	Ser	Ser	Phe	Ser	Thr	Phe	His	Leu	Tyr	Leu	Thr	Leu	Asn	Phe	
380					385					390					395	

CTC CTT CCT TTG AAG GTA CTG GAG ATA GCA AAT ACA ATA TTC TGC CAA	1312
Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln	
400 405 410	
 TGG TTC AAG GGT AAG TAC ATG GAT CTT AAA AGG AAG ACG AGG TTG TTG	1360
Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu	
415 420 425	
 TTG CGT TTA GTA GAC ATT TAT AAA CCC TAC CTC TTC TTC CAA GGC ATC	1408
Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile	
430 435 440	
 TTT GAT GAC ATG AAC ACT GAG AAG TTG CGG ATT GCT GCA AAA GAA AGC	1456
Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser	
445 450 455	
 ATA GTT GAA GCT GAT ATG TTT TAC TTT GAT CCC AGG GCA ATT AAC TGG	1504
Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp	
460 465 470 475	
 GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT	1552
Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val	
480 485 490	
 CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN	1608
Leu Asn	
 NCAACATAAA AGACGTGGTT AAAGTCATGG TCAAAAAAGA AATAAAATGC AGTTAGGTTT	1668
 GTGTTGCAGT TTTGATTCCT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTTTTTTAAT	1728
 GAAATTTCTC TCTTTGTTTT GTGAAAAAAA AAAAAAAAAA GAGCTCCTGC AGAAGCTT	1786

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 :

```
GGAACTCCAT CCCTTCCTCC CTCACTCCTC TCTCTACA ATG AAG GCC AAA ACA ATC 56
                                   Met Lys Ala Lys Thr Ile
                                   1       5

ACA AAC CCG GAG ATC CAA GTC TCC ACG ACC ATG ACC ACC ACG ACC ACG 104
Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
      10              15              20

ACT ATG ACC GCC ACT CTC CCC AAC TTC AAG TCC TCC ATC AAC TTA CAC 152
Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His
      25              30              35

CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC TCC AAT GCC CTC TTC CTC 200
His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu
      40              45              50

GTA TTC ATC CCC CTT TTG GGC CTC GCT TCG GCC CAT CTC TCC TCC TTC 248
Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His Leu Ser Ser Phe
      55              60              65              70

TCG GCC CAT GAC TTG TCC CTG CTC TTC GAC CTC CTT CGC CGC AAC CTC 296
Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu
      75              80              85

CTC CCT GTT GTC GTT TGT TCT TTC CTC TTC GTT TTA TTA GCA ACC CTA 344
Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu
      90              95              100

CAT TTC TTG ACC CGG CCC AGG AAT GTC TAC TTG GTG GAC TTT GGA TGC 392
His Phe Leu Thr Arg Pro Arg Asn Val Tyr Leu Val Asp Phe Gly Cys
      105              110              115

TAT AAG CCT CAA CCG AAC CTG ATG ACA TCC CAC GAG ATG TTC ATG GAC 440
Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser His Glu Met Phe Met Asp
      120              125              130
```

CGG ACC TCC CGG GCC GGG TCG TTT TCT AAG GAG AAT ATT GAG TTT CAG	488
Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys Glu Asn Ile Glu Phe Gln	
135 140 145 150	
AGG AAG ATC TTG GAG AGG GCC GGT ATG GGT CGG GAA ACC TAT GTC CCC	536
Arg Lys Ile Leu Glu Arg Ala Gly Met Gly Arg Glu Thr Tyr Val Pro	
155 160 165	
GAA TCC GTC ACT AAG GTG CCC GCC GAG CCG AGC ATA GCA GCA GCC AGG	584
Glu Ser Val Thr Lys Val Pro Ala Glu Pro Ser Ile Ala Ala Ala Arg	
170 175 180	
GCC GAG GCG GAG GAG GTG ATG TAC GGG GCG ATC GAC GAG GTG TTG GAG	632
Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu	
185 190 195	
AAG ACG GGG GTG AAG CCG AAG CAG ATA GGA ATA CTG GTG GTG ANC TGC	680
Lys Thr Gly Val Lys Pro Lys Gln Ile Gly Ile Leu Val Val Xxx Cys	
200 205 210	
AGC TTG TTT AAC CCA ACG CCG TCG CTG TCA TCC ATG ATA GTT AAC CAT	728
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His	
215 220 225 230	
TAC AAG CTN AGG GGT AAT ATA CTT AGC TAT AAT CTT GGT GGC ATG GGT	776
Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly	
235 240 245	
TGC AGT GCT GGG CTC ATT TCC ATT GAT CTT GCC AAG GAC CTC CTA CAG	824
Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala Lys Asp Leu Leu Gln	
250 255 260	
GTT TAC CGT AAA AAC ACA TAT GTG TTA GTA GTG AGC ACG GAA AAC ATG	872
Val Tyr Arg Lys Asn Thr Tyr Val Leu Val Val Ser Thr Glu Asn Met	
265 270 275	
ACC CTT AAT TGG TAC TGG GGC AAT GAC CGC TCC ATG CTT ATC ACC AAC	920
Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser Met Leu Ile Thr Asn	
280 285 290	
TGC CTA TTT CGC ATG GGT GGC GCT GCC ATC ATC CTC TCA AAC CGC TGG	968
Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile Leu Ser Asn Arg Trp	
295 300 305 310	



CGT	GAT	CGT	CGC	CGA	TCC	AAG	TAC	CAA	CTC	CTT	CAT	ACA	GTA	CGC	ACC	1016
Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Gln	Leu	Leu	His	Thr	Val	Arg	Thr	
				315					320					325		
CAC	AAG	GGC	GCT	GAC	GAC	AAG	TCC	TAT	AGA	TGC	GTC	TTA	CAA	CAA	GAA	1064
His	Lys	Gly	Ala	Asp	Asp	Lys	Ser	Tyr	Arg	Cys	Val	Leu	Gln	Gln	Glu	
			330					335					340			
GAT	GAA	AAT	AAC	AAG	GTA	GGT	GTT	GCC	TTA	TCC	AAG	GAT	CTG	ATG	GCA	1112
Asp	Glu	Asn	Asn	Lys	Val	Gly	Val	Ala	Leu	Ser	Lys	Asp	Leu	Met	Ala	
		345					350					355				
GTT	GCC	GGT	GAA	GCC	CTA	AAG	GCC	AAC	ATC	ACG	ACC	CTT	GGT	CCC	CTC	1160
Val	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	
	360					365					370					
GTG	CTC	CCC	ATG	TCA	GAA	CAA	CTC	CTC	TTC	TTT	GCC	ACC	TTA	GTG	GCA	1208
Val	Leu	Pro	Met	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Thr	Leu	Val	Ala	
375					380				385						390	
CGT	AAG	GTC	TTC	AAG	ATG	ACG	AAC	GTG	AAG	CCA	TAC	ATC	CCA	GAT	TTC	1256
Arg	Lys	Val	Phe	Lys	Met	Thr	Asn	Val	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	
				395				400						405		
AAG	TTG	GCA	GCG	AAC	GAC	TTC	TGC	ATC	CAT	GCA	GGA	GGC	AAA	GCA	GTG	1304
Lys	Leu	Ala	Ala	Asn	Asp	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	
			410					415					420			
TTG	GAT	GAG	CTC	GAG	AAG	AAC	TTG	GAG	TTG	ACG	CCA	TGG	CAC	CTT	GAA	1352
Leu	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Glu	Leu	Thr	Pro	Trp	His	Leu	Glu	
		425					430					435				
CCC	TCG	AGG	ATG	ACA	CTG	TAT	AGG	TTT	GGG	AAC	ACA	TCG	AGT	AGC	TCA	1400
Pro	Ser	Arg	Met	Thr	Leu	Tyr	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	
	440					445					450					
TTA	TGG	TAC	GAG	TTG	GCA	TAC	GCT	GAA	GCA	AAA	GGG	AGG	ATC	CGT	AAG	1448
Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ala	Glu	Ala	Lys	Gly	Arg	Ile	Arg	Lys	
455					460					465					470	

GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC 1496  
 Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn  
                     475                    480                    485

AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG 1544  
 Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys  
                     490                    495                    500

AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA 1592  
 Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys  
                     505                    510                    515

ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA 1640  
 Ile Ala Pro Ile Ala Ser  
                     520

AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAACTTTA GTTGATGGGT GAGAACATGT 1700  
 CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG 1733

(2) INFORMATION FOR SEQ ID NO:3 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1783 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 :

GTCGACACA ATG AAG GCC AAA ACA ATC ACA AAC CCG GAG ATC CAA GTC TCC 51  
           Met Lys Ala Lys Thr Ile Thr Asn Pro Glu Ile Gln Val Ser  
           1                    5                    10

ACG ACC ATG ACC ACC ACG ACC ACG ACC GCC ACT CTC CCC AAC TTC AAG 99  
 Thr Thr Met Thr Thr Thr Thr Thr Thr Thr Ala Thr Leu Pro Asn Phe Lys  
 15                    20                    25                    30

TCC	TCC	ATC	AAC	TTA	CAC	CAC	GTC	AAG	CTC	GGC	TAC	CAC	TAC	TTA	ATC	147
Sér	Sér	Ile	Asn	Leu	His	His	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	
			35					40						45		
TCC	AAT	GCC	CTC	TTC	CTC	GTA	TTC	ATC	CCC	CTT	TTG	GGC	CTC	GCT	TCG	195
Sér	Asn	Ala	Leu	Phe	Leu	Val	Phe	Ile	Pro	Leu	Leu	Gly	Leu	Ala	Sér	
			50					55					60			
GCC	CAC	CTC	TCC	TCC	TTC	TCG	GCC	CAT	GAC	TTG	TCC	CTG	CTC	TTC	GAC	243
Ala	His	Leu	Sér	Sér	Phe	Sér	Ala	His	Asp	Leu	Sér	Leu	Leu	Phe	Asp	
		65					70					75				
CTC	CTT	CGC	CGC	AAC	CTC	CTC	CCC	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	291
Leu	Leu	Arg	Arg	Asn	Leu	Leu	Pro	Val	Val	Val	Cys	Sér	Phe	Leu	Phe	
	80					85					90					
GTT	TTA	TTA	GCA	ACC	CTA	CAT	TTC	TTG	ACC	CGG	CCT	AGG	AAT	GTC	TAC	339
Val	Leu	Leu	Ala	Thr	Leu	His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	
95					100				105						110	
TTG	GTG	GAC	TTT	GCC	TGC	TAT	AAG	CCT	CAC	CCG	AAC	CTG	ATA	ACA	TCC	387
Leu	Val	Asp	Phe	Ala	Cys	Tyr	Lys	Pro	His	Pro	Asn	Leu	Ile	Thr	Sér	
				115					120					125		
CAC	GAG	ATG	TTC	ATG	GAC	CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	435
His	Glu	Met	Phe	Met	Asp	Arg	Thr	Sér	Arg	Ala	Gly	Sér	Phe	Sér	Lys	
			130					135					140			
GAG	AAT	ATT	GAG	TTT	CAG	AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGC	483
Glu	Asn	Ile	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	
		145					150					155				
CGG	GAA	ACC	TAC	GTC	CCC	GAA	TCC	GTC	ACT	AAG	GTG	CCG	CCC	GAG	CCG	531
Arg	Glu	Thr	Tyr	Val	Pro	Glu	Sér	Val	Thr	Lys	Val	Pro	Pro	Glu	Pro	
	160					165					170					
AGC	ATA	GCA	GCA	GCC	AGG	GCC	GAG	GCG	GAG	GAG	GTG	ATG	TAC	GGG	GCG	579
Sér	Ile	Ala	Ala	Ala	Arg	Ala	Glu	Ala	Glu	Glu	Val	Met	Tyr	Gly	Ala	
175					180				185						190	
ATC	GAC	GAG	GTG	TTG	GAG	AAG	ACG	GGG	GTG	AAG	CCG	AAG	CAG	ATA	GGA	627
Ile	Asp	Glu	Val	Leu	Glu	Lys	Thr	Gly	Val	Lys	Pro	Lys	Gln	Ile	Gly	
				195				200						205		

ATA	CTG	GTG	GTG	AAC	TGC	AGC	TTG	TTT	AAC	CCA	ACG	CCG	TCG	CTG	TCA	675
Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	
		210						215					220			
TCC	ATG	ATA	GTT	AAC	CAT	TAC	AAG	CTT	AGG	GGT	AAT	ATA	CTT	AGC	TAT	723
Ser	Met	Ile	Val	Asn	His	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	
		225					230					235				
AAT	CTT	GGT	GGC	ATG	GGT	TGC	AGT	GCT	GGG	CTC	ATT	TCC	ATT	GAT	CTT	771
Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Leu	Ile	Ser	Ile	Asp	Leu	
	240					245					250					
GCC	AAG	GAC	CTC	CTA	CAG	GTT	TAC	CGT	AAC	ACA	TAT	GTG	TTA	GTA	GTG	819
Ala	Lys	Asp	Leu	Leu	Gln	Val	Tyr	Arg	Asn	Thr	Tyr	Val	Leu	Val	Val	
255					260					265					270	
AGC	ACA	GAA	AAC	ATG	ACC	CTT	AAT	TGG	TAC	TGG	GGC	AAT	GAC	CGC	TCC	867
Ser	Thr	Glu	Asn	Met	Thr	Leu	Asn	Trp	Tyr	Trp	Gly	Asn	Asp	Arg	Ser	
			275					280						285		
ATG	CTT	ATC	ACC	AAC	TGC	CTA	TTT	CGC	ATG	GGT	GGC	GCT	GCC	ATC	ATC	915
Met	Leu	Ile	Thr	Asn	Cys	Leu	Phe	Arg	Met	Gly	Gly	Ala	Ala	Ile	Ile	
			290					295					300			
CTC	TCA	AAC	CGC	TGG	CGT	GAT	CGT	CGC	CGA	TCC	AAG	TAC	CAA	CTC	CTT	963
Leu	Ser	Asn	Arg	Trp	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Gln	Leu	Leu	
		305					310					315				
CAC	ACA	GTA	CGC	ACC	CAC	AAG	GGC	GCT	GAC	GAC	AAG	TCC	TAT	AGA	TGC	1011
His	Thr	Val	Arg	Thr	His	Lys	Gly	Ala	Asp	Asp	Lys	Ser	Tyr	Arg	Cys	
	320					325					330					
GTC	TTA	CAA	CAA	GAA	GAT	GAA	AAT	AAC	AAG	GTA	GGT	GTT	GCC	TTA	TCC	1059
Val	Leu	Gln	Gln	Glu	Asp	Glu	Asn	Asn	Lys	Val	Gly	Val	Ala	Leu	Ser	
335					340					345					350	
AAG	GAT	CTG	ATG	GCA	GTT	GCC	GGT	GAA	GCC	CTA	AAG	GCC	AAC	ATC	ACG	1107
Lys	Asp	Leu	Met	Ala	Val	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	
				355					360					365		

ACC CTT GGT CCC CTC GTG CTC CCC ATG TCA GAA CAA CTC CTC TTC TTT 1155  
 Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe  
 370 375 380

GCC ACC TTA GTG GCA CGT AAG GTC TTC AAG ATG ACG AAC GTG AAG CCA 1203  
 Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro  
 385 390 395

TAC ATC CCA GAT TTC AAG TTG GCA GCG AAG CAC TTC TGC ATC CAT GCA 1251  
 Tyr Ile Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala  
 400 405 410

GGA GGC AAA GCA GTG TTG GAT GAG CTC GAG ACG AAC TTG GAG TTG ACG 1299  
 Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr  
 415 420 425 430

CCA TGG CAC CTT GAA CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC 1347  
 Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn  
 435 440 445

ACA TCG AGT AGC TCA TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA 1395  
 Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys  
 450 455 460

GGG AGG ATC CGT AAG GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA 1443  
 Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser  
 465 470 475

GGT TTC AAG TGT AAC AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT 1491  
 Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn  
 480 485 490

CCG GCT AGA GAG AAG AAT CCT TGG ATG GAT GAA ATT GAG AAT TTC CCT 1539  
 Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro  
 495 500 505 510

GTC CAT GTG CCT AAA ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT 1592  
 Val His Val Pro Lys Ile Ala Pro Ile Ala Ser  
 515 520

TAGTAATGAA AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT 1652

GAGAACATGT CTCATTGAGA ATAACGTGTG CATCGTTGTG TTGAATTTGA ATTTGAGTAT 1712  
 TGGTGAAATT CTGTTAGAAT TGACGCATGA GTCATATATA TACAAATTTA AGTAAGATTT 1772  
 TACGCTTTCT T 1783

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1647 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: PCR to genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4 :

GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA 60  
 AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC 120  
 GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCATG 180  
 GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCTC TGGTACGCCA ATTCCGCTCC 240  
 CCAGAAGCAA CCGGCGCCGA ATTGCGCGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC 300  
 GGGTCCTTGC GCGATTGCGG CGGAAGCCGG GTCGGGTTGG GGACGAGACC CGAATCCGAG 360  
 CCTGGTGAAG AGGTTGTTCA TCGGAGATTT ATAGACGGAG ATGGATCGAG CGGTTTTGGG 420  
 GAAAGGGGAA GTGGGTTTGG CTCTTTTGGG TAGAGAGAGT GCAGCTTTGG AGAGAGACTG 480  
 GAGAGGTTTA GAGAGAGACG CGGCGGATAT TACCGGAGGA GAGGCGACGA GAGATAGCAT 540  
 TATCGAAGGG GAGGGAGAAA GAGTGACGTG GAGAAATAAG AAACCGTTAA GAGTCGGATA 600

TTTATCATAT TAAAAGCCCA ATGGGCCTGA ACCCATTTAA ACAAGACAGA TAAATGGGCC 660  
 GTGTGTTAAG TTAACAGAGT GTTAACGTTT GGTTCCTAAAT GCCAACGCCA TAGGAACAAA 720  
 ACAAACGTGT CCTCAAGTAA ACCCCTGCCG TTTACACCTC AATGGCTGCA TGGTGAAGCC 780  
 ATTAACACGT GCGTAGGAT GCATGACGAC GCCATTGACA CCTGACTCTC TTCCCTTCTC 840  
 TTCATATATC TCTAATCAAT TCAACTACTC ATTGTCATAG CTATTCGGAA AATACATACA 900  
 CATCCTTTTC TCTTCGATCT CTCTCAATTC ACAAGAAGCA AAGTCGACGG ATCCCTGCAG 960  
 TAAATTACGC CATGACTATT TTCATAGTCC AATAAGGCTG ATGTCGGGAG TCCAGTTTAT 1020  
 GAGCAATAAG GTGTTTAGAA TTTGATCAAT GTTTATAATA AAAGGGGGAA GATGATATCA 1080  
 CAGTCTTTTG TTCTTTTTGG CTTTTGTTAA ATTTGTGTGT TTCTATTTGT AAACCTCCTG 1140  
 TATATGTTGT ACTTCTTTCC CTTTTTAAGT GGTATCGTCT ATATGGTAAA ACGTTATGTT 1200  
 TGGTCTTTCC TTTTCTCTGT TTAGGATAAA AAGACTGCAT GTTTTATCTT TAGTTATATT 1260  
 ATGTTGAGTA AATGAACTTT CATAGATCTG GTTCCGTAGA GTAGACTAGC AGCCGAGCTG 1320  
 AGCTGAACTG AACAGCTGGC AATGTGAACA CTGGATGCAA GATCAGATGT GAAGATCTCT 1380  
 AATATGGTGG TGGGATTGAA CATATCGTGT CTATATTTTT GTTGGCATTG AGCTCTTAAC 1440  
 ATAGATATAA CTGATGCAGT CATTGGTTCA TACACATATA TAGTAAGGAA TTACAATGGC 1500  
 AACCCAACT TCAAAAACAG TAGGCCACCT GAATTGCCTT ATCGAATAAG AGTTTGTTC 1560  
 CCCCCACTTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620  
 GCAGAACCTC TAGAGGTACC GGCGCGC 1647

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 :

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys  
5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6 :

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa  
5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

Glu Thr Tyr Val Pro Glu Glu Val Thr Lys  
5 10



(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 :

Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys  
                    5                    10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9 :

Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe  
                    5                    10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10 :

Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu  
                    5                    10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala  
                    5                    10                    15  
Lys

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 :

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu  
                    5                    10                    15  
Lys

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 :

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala  
5 10 15  
Xaa Ile Leu Lys Asp Ala Gly  
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 :

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser  
5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :

AAAYATHACNA CNYTNGG

17

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other
  - (A) DESCRIPTION: synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :

17

SWRTTRCAYT TRAANCC

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1810 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 :

GAA	ATG	AGT	AGG	TCT	AGC	GAA	CAA	GAT	CTA	CTC	TCT	ACC	GAG	ATT	GTT	48
Met	Ser	Arg	Ser	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Thr	Glu	Ile	Val	15	
1					5					10						

AAC	CGT	GGG	ATC	GAA	CCT	TCC	GGT	CCA	AAC	GCC	GGT	TCA	CCA	ACG	TTC	96
Asn	Arg	Gly	Ile	Glu	Pro	Ser	Gly	Pro	Asn	Ala	Gly	Ser	Pro	Thr	Phe	
				20					25					30		

TCG	GTC	AGA	GTC	CGG	AGA	CGT	TTA	CCG	GAT	TTT	CTT	CAA	TCC	GTA	AAC	144
Ser	Val	Arg	Val	Arg	Arg	Arg	Leu	Pro	Asp	Phe	Leu	Gln	Ser	Val	Asn	
			35					40					45			

TTG AAG TAC GTG AAA CTT GGT TAT CAC TAC CTC ATA AAC CAT GCG GTT	192
Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val	
50 55 60	
TAC TTG GCG ACG ATA CCG GTT CTT GTG CTT GTG TTT AGT GCC GAA GTT	240
Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val	
65 70 75	
GGG AGT TTA AGC GGA GAA GAG ATT TGG AAG AAG CTT TGG GAC TAT GAT	288
Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp	
80 85 90 95	
ATC GCA ACC GTC ATC GGA TTC TTC GGT GTC TTT GTC TTG ACC GTT TGC	336
Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys	
100 105 110	
GTC TAC TTC ATG TCT CGT CCA CGA TCT GTT TAT CTC ATT GAC TTC GCT	384
Val Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala	
115 120 125	
TGT TTC AAG CCT TCC GAT GAA CTT AAG GTG ACA AGA GAA GAG TTC ATA	432
Cys Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile	
130 135 140	
GAT CTA GCT AGA AAA TCA GGC AAG TTC GAC GAA GAG ATC CTC GGA TTC	480
Asp Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe	
145 150 155	
AAG AAG AGG ATC CTT CAA GCC TCA GGA ATA GGC GAT GAA ACG TAC GTC	528
Lys Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val	
160 165 170 175	
CCA AGA TCA ATC TCT TCG TCG GAA AAC ACA ACA ACG ATG AAA GAA GGT	576
Pro Arg Ser Ile Ser Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly	
180 185 190	
CGT GAA GAA GCC TCG ATG ATG ATA TTC GGC GCA CTC GAC GAA CTC TTC	624
Arg Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe	
195 200 205	
GAG AAG ACA CGT GTC AAA CCG AAA GAC GTA GGT GTC CTC GTG GTT AAC	672
Glu Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn	
210 215 220	

TGC	AGT	ATC	TTT	AAC	CCG	ACT	CCG	TCA	CTC	TCC	GCG	ATG	GTG	ATT	AAC	720
Cys	Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	
	225					230					235					
CAC	TAC	AAG	ATG	AGA	GGG	AAC	ATA	CTT	AGC	TAC	AAC	CTA	GGA	GGG	ATG	768
His	Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	
240					245					250					255	
GGT	TGC	TCA	GCA	GGA	ATC	ATA	GCC	GTT	GAT	CTT	GCT	CGT	GAC	ATG	CTT	816
Gly	Cys	Ser	Ala	Gly	Ile	Ile	Ala	Val	Asp	Leu	Ala	Arg	Asp	Met	Leu	
				260					265					270		
CAG	TCT	AAC	CCG	AAT	AGT	TAC	GCG	GTG	GTT	GTG	AGT	ACC	GAG	ATG	GTT	864
Gln	Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	
			275					280					285			
GGG	TAT	AAT	TGG	TAC	GTG	GGA	CGT	GAC	AAG	TCA	ATG	GTT	ATA	CCT	AAC	912
Gly	Tyr	Asn	Trp	Tyr	Val	Gly	Arg	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	
		290					295					300				
TGC	TTC	TTT	AGG	ATG	GGT	TGC	TCC	GCC	GTT	ATG	CTG	TCT	AAC	CGC	CGC	960
Cys	Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	
	305					310					315					
CGT	GAC	TTC	CGC	CAT	GCT	AAG	TAC	CGC	CTT	GAG	CAC	ATT	GTC	CGG	ACT	1008
Arg	Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	
320					325					330					335	
CAC	AAG	GCT	GCC	GAC	GAC	CGT	AGC	TTC	AGG	AGT	GTG	TAC	CAG	GAA	GAA	1056
His	Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	
				340					345					350		
GAT	GAA	CAA	GGA	TTC	AAG	GGA	TTA	AAA	ATA	AGC	AGA	GAC	CTA	ATG	GAA	1104
Asp	Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	
			355					360					365			
GTT	GGA	GGT	GAA	GCT	CTC	AAG	ACC	AAC	ATC	ACC	ACC	TTA	GGC	CCT	CTC	1152
Val	Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	
		370					375					380				

GTC	CTT	CCT	TTC	TCC	GAG	CAG	CTT	CTC	TTC	TTT	GCC	GCT	TTG	ATC	CGT	1200	
Val	Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Ile	Arg		
	385					390					395						
AGA	ACT	TTC	TCA	CCC	GCC	GCC	AAA	ACT	ACC	ACC	ACC	TCC	TCC	TCA	GCC	1248	
Arg	Thr	Phe	Ser	Pro	Ala	Ala	Lys	Thr	Thr	Thr	Thr	Ser	Ser	Ser	Ala		
400					405					410					415		
ACT	GCG	AAA	ATC	AAC	GGA	GCC	AAG	TCG	TCA	TCC	TCC	TCT	GAT	CTA	TCC	1296	
Thr	Ala	Lys	Ile	Asn	Gly	Ala	Lys	Ser	Ser	Ser	Ser	Ser	Asp	Leu	Ser		
				420				425						430			
AAG	CCG	TAC	ATC	CCG	GAC	TAC	AAG	CTT	GCC	TTC	GAG	CAT	TTC	TGC	TTC	1344	
Lys	Pro	Tyr	Ile	Pro	Asp	Tyr	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Phe		
			435					440					445				
CAC	GCG	GCA	AGC	AAA	GCG	GTG	CTT	GAG	GAG	CTT	CAG	AAG	AAT	CTA	GGC	1392	
His	Ala	Ala	Ser	Lys	Ala	Val	Leu	Glu	Glu	Leu	Gln	Lys	Asn	Leu	Gly		
		450					455					460					
TTG	AGT	GAT	GAG	AAC	ATG	GAG	GCT	TCT	AAG	ATG	ACT	TTA	CAC	AGG	TTT	1440	
Leu	Ser	Asp	Glu	Asn	Met	Glu	Ala	Ser	Lys	Met	Thr	Leu	His	Arg	Phe		
	465					470					475						
GGA	AAC	ACT	TCC	AGC	AGT	GGA	ATC	TGG	TAC	GAG	CTT	GCT	TAC	ATG	GAG	1488	
Gly	Asn	Thr	Ser	Ser	Ser	Gly	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Met	Glu		
480					485					490					495		
GCC	AAG	GAG	AGT	GTT	CGT	AGA	GGC	GAT	AGG	GTT	TGG	CAG	ATT	GCT	TTT	1536	
Ala	Lys	Glu	Ser	Val	Arg	Arg	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala	Phe		
				500					505					510			
GGG	TCA	GGT	TTT	AAG	TGT	AAC	AGT	GTG	GTT	TGG	AAG	GCA	ATG	AGG	AAG	1584	
Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Val	Val	Trp	Lys	Ala	Met	Arg	Lys		
			515					520					525				
GTG	AAG	AAG	CCG	GCA	AGG	AAC	AAT	CCT	TGG	GTT	GAT	TGC	ATT	AAC	CGT	1632	
Val	Lys	Lys	Pro	Ala	Arg	Asn	Asn	Pro	Trp	Val	Asp	Cys	Ile	Asn	Arg		
		530					535					540					
TAC	CCT	GTC	GCT	CTC	TGATCATTTA	TTTTTAAAAT	TATTATTTCT	TCTTAATTAA								1687	
Tyr	Pro	Val	Ala	Leu													
	545																

ATCATCTATG ATCTCTCTTC CTTGTTGTTG GATGATAGAC GTTTGTTTGC TGGTCATTCG 1747  
TATCTTAAGA CTTCTATAAG AATGGATGGT TCAAGTCCAA AAAAAAAAAA AAAAAAAAAA 1807  
AAA 1810

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 :

GTCGACAAA ATG ACG TCC ATT AAC GTA AAG CTC CTT TAC CAT TAC GTC ATA 51  
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile  
1 5 10

ACC AAC CTT TTC AAC CTT TGT TTC TTT CCA TTA ACG GCG ATC GTC GCC 99  
Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala  
15 20 25 30

GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT 147  
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr  
35 40 45

TCC TAT CTC CAA CAC AAC CTC ATA ACC ATT GCT CCA CTC TTT GCC TTC 195  
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe  
50 55 60

ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT 243  
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val  
65 70 75

TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA 291  
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser  
80 85 90



AGT	ATC	TCC	AAG	GTC	ATG	GAT	ATC	TTT	TAC	CAA	GTA	AGA	AAA	GCT	GAT	339
Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	
95					100					105					110	
CCT	TCT	CGG	AAC	GGC	ACG	TGC	GAT	GAC	TCG	TCC	TGG	CTT	GAC	TTC	TTG	387
Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	
				115					120					125		
AGG	AAG	ATT	CAA	GAA	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACC	CAC	GGG	CCC	435
Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	
			130					135					140			
GAG	GGG	CTG	CTT	CAG	GTC	CCT	CCC	CGG	AAG	ACT	TTT	GCG	GCG	GCG	CGT	483
Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	
		145					150					155				
GAA	GAG	ACG	GAG	CAA	GTT	ATC	ATT	GGT	GCG	CTA	GAA	AAT	CTA	TTC	AAG	531
Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	
	160					165					170					
AAC	ACC	AAT	GTT	AAC	CCT	AAA	GAT	ATA	GGT	ATA	CTT	GTG	GTG	AAC	TCA	579
Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	
175					180				185						190	
AGC	ATG	TTT	AAT	CCA	ACT	CCT	TCG	CTC	TCC	GCG	ATG	GTC	GTT	AAC	ACT	627
Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	
				195					200					205		
TTC	AAG	CTC	CGA	AGC	AAC	GTA	AGA	AGC	TTT	AAC	CTT	GGT	GGC	ATG	GGT	675
Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	
			210					215					220			
TGT	AGT	GCC	GGC	GTT	ATA	GCC	ATT	GAT	CTA	GCA	AAG	GAC	TTG	TTG	CAT	723
Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	
		225					230					235				
GTC	CAT	AAA	AAT	ACG	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	771
Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	
	240					245					250					

TAT	AAC	ATT	TAC	GCT	GGT	GAT	AAT	AGG	TCC	ATG	ATG	GTT	TCA	AAT	TGC	819
Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	
255					260					265					270	
TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	AGA	867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Arg	
				275					280						285	
GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT	915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	
				290				295						300		
ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GTT	963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Val	
		305					310						315			
GAG	AAC	GGC	AAA	ACC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT	1011
Glu	Asn	Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	
	320					325					330					
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	CTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345					350	
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
				355					360					365		
AAA	CTT	TTC	AAA	GAC	AAA	ATC	AAA	CAT	TAT	TAC	GTC	CCG	GAC	TTC	AAG	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
			370					375					380			
CTT	GCT	ATC	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AAA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	Ile	
		385					390					395				
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GGC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
	400					405					410					
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415					420					425					430	

TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
				435					440					445		

AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
			450					455					460			

GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC			1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys				
		465					470					475				

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 :

GTCGACAAA	ATG	ACG	TCC	ATT	AAC	GTA	AAG	CTC	CTT	TAC	CAT	TAC	GTC	ATA	51
	Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	
	1				5					10					

ACC	AAC	CTT	TTC	AAC	CTT	TGC	TTC	TTT	CCG	TTA	ACG	GCG	ATC	GTC	GCC	99
Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	
15					20					25				30		

GGA	AAA	GCC	TAT	CGG	CTT	ACC	ATA	GAC	GAT	CTT	CAC	CAC	TTA	TAC	TAT	147
Gly	Lys	Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	
				35				40					45			

TCC	TAT	CTC	CAA	CAC	AAC	CTC	ATA	ACC	ATC	GCT	CCA	CTC	TTT	GCC	TTC	195
Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	
			50					55					60			

AAC	GTT	TTC	GGT	TCG	GTT	CTC	TAC	ATC	GCA	ACC	CGG	CCC	AAA	CCG	GTT	243
Thr	Val	Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	
	65					70					75					
TAC	CTC	GTT	GAG	TAC	TCA	TGC	TAC	CTT	CCA	CCA	ACG	CAT	TGT	AGA	TCA	291
Tyr	Leu	Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	
	80					85					90					
AGT	ATC	TCC	AAG	GTC	ATG	GAT	ATC	TTT	TAT	CAA	GTA	AGA	AAA	GCT	GAT	339
Ser	Ile	Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	
95					100					105					110	
CCT	TCT	CGG	AAC	GGC	ACG	TGC	GAT	GAC	TCG	TCG	TGG	CTT	GAC	TTC	TTG	387
Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	
				115					120					125		
AGG	AAG	ATT	CAA	GAA	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACT	CAC	GGG	CCC	435
Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	
			130					135						140		
GAG	GGG	CTG	CTT	CAG	GTC	CCT	CCC	CGG	AAG	ACT	TTT	GCG	GCG	GCG	CGT	483
Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	
		145					150					155				
GAA	GAG	ACG	GAG	CAA	GTT	ATC	ATT	GGT	GCG	CTA	GAA	AAT	CTA	TTC	AAG	531
Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	
	160					165					170					
AAC	ACC	AAC	GTT	AAC	CCT	AAA	GAT	ATA	GGT	ATA	CTT	GTG	GTG	AAC	TCA	579
Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	
175					180					185					190	
AGC	ATG	TTT	AAT	CCA	ACT	CCA	TCG	CTC	TCC	GCG	ATG	GTC	GTT	AAC	ACT	627
Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	
				195					200					205		
TTC	AAG	CTC	CGA	AGC	AAC	GTA	AGA	AGC	TTT	AAC	CTT	GGT	GGC	ATG	GGT	675
Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	
			210					215					220			

TGT	AGT	GCC	GGC	GTT	ATA	GCC	ATT	GAT	CTA	GCA	AAG	GAC	TTG	TTG	CAT	723
Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	
		225					230					235				
GTC	CAT	AAA	AAT	ACG	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	771
Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	
		240				245					250					
TAT	AAC	ATT	TAC	GCT	GGT	GAT	AAT	AGG	TCC	ATG	ATG	GTT	TCA	AAT	TGC	819
Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	
255					260					265					270	
TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	GGA	867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	
				275					280					285		
GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT	915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	
				290				295					300			
ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GAT	963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	
		305					310					315				
GAG	AAC	GGC	AAA	ATC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT	1011
Glu	Asn	Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	
	320					325					330					
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	TTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345					350	
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
				355					360					365		
AAA	CTT	TTC	AAA	GAT	AAA	ATC	AAA	CAT	TAC	TAC	GTC	CCG	GAT	TTC	AAA	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
			370					375					380			
CTT	GCT	ATT	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AGA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	
		385					390					395				

GAT	GTG	CTA	GAG	AAG	AAC	CTA	GCC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
	400					405					410					

TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415					420					425					430	

TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
			435						440					445		

AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
		450						455					460			

GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC			1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys				
		465				470						475				

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 :

AAG	CTT	AAA	CTA	GTG	TAT	CAT	TAC	CTA	ATC	TCC	AAC	GCT	CTC	TAC	ATC	48
Lys	Leu	Lys	Leu	Val	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Ala	Leu	Tyr	Ile	
1				5					10					15		

CTC	CTC	CTT	CCT	CTC	CTC	GCC	GCA	ACA	ATC	GCT	AAC	CTC	TCT	TCT	TTC	96
Leu	Leu	Leu	Pro	Leu	Leu	Ala	Ala	Thr	Ile	Ala	Asn	Leu	Ser	Ser	Phe	
			20					25					30			

ACC	ATC	AAC	GAC	CTC	TCT	CTC	CTC	TAC	AAC	ACA	CTC	CGT	TTC	CAT	TTC	144
Thr	Ile	Asn	Asp	Leu	Ser	Leu	Leu	Tyr	Asn	Thr	Leu	Arg	Phe	His	Phe	
		35					40					45				
CTC	TCC	GCC	ACA	CTC	GCC	ACC	GCA	CTC	TTG	ATC	TCT	CTC	TCC	ACC	GCT	192
Leu	Ser	Ala	Thr	Leu	Ala	Thr	Ala	Leu	Leu	Ile	Ser	Leu	Ser	Thr	Ala	
	50					55					60					
TAC	TTC	ACC	ACC	CGT	CCT	CGC	CGT	GTC	TTC	CTC	CTC	GAC	TTC	TCG	TGT	240
Tyr	Phe	Thr	Thr	Arg	Pro	Arg	Arg	Val	Phe	Leu	Leu	Asp	Phe	Ser	Cys	
65					70					75					80	
TAC	AAA	CCA	GAC	CCT	TCA	CTG	ATC	TGC	ACT	CGT	GAA	ACA	TTC	ATG	GAC	288
Tyr	Lys	Pro	Asp	Pro	Ser	Leu	Ile	Cys	Thr	Arg	Glu	Thr	Phe	Met	Asp	
				85					90					95		
AGA	TCT	CAA	CGT	GTA	GGC	ATC	TTC	ACA	GAA	GAC	AAC	TTA	GCT	TTC	CAA	336
Arg	Ser	Gln	Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	
			100					105					110			
CAA	AAG	ATC	CTC	GAA	AGA	TCC	GGT	CTA	GGT	CAG	AAA	ACT	TAC	TTC	CCT	384
Gln	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	
		115					120					125				
GAA	GCT	CTT	CTT	CGT	GTT	CCT	CCT	AAT	CCT	TGT	ATG	GAA	GAA	GCG	AGA	432
Glu	Ala	Leu	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	
	130					135					140					
AAA	GAG	GCA	GAA	ACA	GTT	ATG	TTC	GGA	GCT	ATT	GAC	GCG	GTT	CTT	GAG	480
Lys	Glu	Ala	Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ala	Val	Leu	Glu	
145					150					155					160	
AAG	ACC	GGT	GTG	AAA	CCT	AAA	GAT	ATT	GGA	ATC	CTT	GTG	GTG	AAT	TGT	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165					170					175		
AGC	TTG	TTT	AAT	CCA	ACA	CCG	TCA	CTT	TCT	GCT	ATG	ATT	GTG	AAT	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			

TAT	AAG	CTT	AGA	GGC	AAC	ATT	TTG	AGC	TAT	AAT	TTC	GGC	GGG	ATG	GG	623
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Phe	Gly	Gly	Met	Gly	
	195						200					205				

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

AAG	CTT	AAG	TTA	GGC	TAC	CAC	TAT	CTG	ATC	ACT	CAC	TTT	TTT	AAA	CTC	48
Lys	Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Phe	Phe	Lys	Leu	
1				5				10						15		

ATG	TTC	CTC	CCT	CTA	ATG	GCT	GTT	TTG	TTC	ATG	AAT	GTC	TCA	TTG	TTA	96
Met	Phe	Leu	Pro	Leu	Met	Ala	Val	Leu	Phe	Met	Asn	Val	Ser	Leu	Leu	
			20					25					30			

AGC	CTA	AAC	CAT	CTT	CAG	CTC	TAT	TAC	AAT	TCC	ACC	GGA	TTC	ATC	TTC	144
Ser	Leu	Asn	His	Leu	Gln	Leu	Tyr	Tyr	Asn	Ser	Thr	Gly	Phe	Ile	Phe	
		35					40					45				

GTC	ATC	ACT	CTC	GCC	ATT	GTC	GGA	TCC	ATT	GTC	TTC	TTC	ATG	TCT	CGA	192
Val	Ile	Thr	Leu	Ala	Ile	Val	Gly	Ser	Ile	Val	Phe	Phe	Met	Ser	Arg	
	50					55					60					

CCT	AGA	TCC	ATC	TAC	CTT	CTA	GAT	TAC	TCT	TGC	TAC	CTC	CCG	CCT	TCG	240
Pro	Arg	Ser	Ile	Tyr	Leu	Leu	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Ser	
65					70				75						80	

AGT	CAA	AAA	GTT	AGC	TAC	CAG	AAA	TTC	ATG	AAC	AAC	TCT	AGT	TTG	ATT	288
Ser	Gln	Lys	Val	Ser	Tyr	Gln	Lys	Phe	Met	Asn	Asn	Ser	Ser	Leu	Ile	
				85					90					95		



CAA	GAT	TTC	AGC	GAA	ACT	TCT	CTT	GAG	TTC	CAG	AGG	AAG	ATC	TTG	ATT	336
Gln	Asp	Phe	Ser	Glu	Thr	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Ile	
			100					105					110			
CGC	TCT	GGT	CTC	GGT	GAA	GAG	ACT	TAT	TTA	CCG	GAT	TCT	ATT	CAC	TCT	384
Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Asp	Ser	Ile	His	Ser	
		115					120					125				
ATC	CCT	CCG	CGT	CCT	ACT	ATG	GCT	GCA	GCG	CGT	GAA	GAA	GCG	GAG	CAG	432
Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	Arg	Glu	Glu	Ala	Glu	Gln	
	130					135					140					
GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTT	TTC	GAG	AAT	ACA	AAA	ATC	AAT	480
Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Glu	Asn	Thr	Lys	Ile	Asn	
145					150					155					160	
CCT	AGG	GAG	ATT	GGT	GTT	CTT	GTT	GTG	AAT	TGT	AGT	TTG	TTT	AAC	CCC	528
Pro	Arg	Glu	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	
				165					170					175		
ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTT	AAC	AAG	TAT	AAG	CTT	AGA	GGA	576
Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	
			180					185					190			
AAC	ATT	AAG	AGC	TTT	AAT	CTC	GGC	GGC	ATG	G						607
Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met							
		195				200										

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAG	CTT	AAA	CTG	GGG	TAC	CAC	TAC	CTC	ATT	ACT	CAT	CTC	TTC	AAG	CTC	48
Lys	Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	
1				5				10						15		
TGT	TTG	GTT	CCA	TTA	ATG	GCG	GTT	TTA	GTC	ACA	GAG	ATC	TCC	CGA	TTA	96
Cys	Leu	Val	Pro	Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	
			20					25					30			
ACA	ACA	GAC	GAT	CTT	TAC	CAG	ATT	TGC	CTT	CAT	CTC	CAA	TAC	AAT	CTC	144
Thr	Thr	Asp	Asp	Leu	Tyr	Gln	Ile	Cys	Leu	His	Leu	Gln	Tyr	Asn	Leu	
		35					40					45				
GTT	GCT	TTC	ATC	TTT	CTC	TCT	GCT	TTA	GCT	ATC	TTT	GGC	TCC	ACC	GTT	192
Val	Ala	Phe	Ile	Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	
	50					55					60					
TAC	ATC	ATG	AGT	CGT	CCC	AGA	TCT	GTT	TAT	CTC	GTT	GAT	TAC	TCT	TGT	240
Tyr	Ile	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	
65					70					75					80	
TAT	CTT	CCT	CCG	GAG	AGT	CTT	CAG	GTT	AAG	TAT	CAG	AAG	TTT	ATG	GAT	288
Tyr	Leu	Pro	Pro	Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	
				85				90						95		
CAT	TCT	AAG	TTG	ATT	GAA	GAT	TTC	AAT	GAG	TCA	TCT	TTA	GAG	TTT	CAG	336
His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	
			100					105					110			
AGG	AAG	ATT	CTT	GAA	CGT	TCT	GGT	TTA	GGA	GAA	GAG	ACT	TAT	CTC	CCT	384
Arg	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	
		115					120					125				
GAA	GCT	TTA	CAT	TGT	ATC	CCT	CCG	AGG	CCT	ACG	ATG	ATG	GCG	GCT	CGT	432
Glu	Ala	Leu	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Met	Ala	Ala	Arg	
	130					135					140					
GAG	GAA	GCT	GAG	CAG	GTA	ATG	TTT	GGT	GCT	CTT	GAT	AAG	CTT	TTC	GAG	480
Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Lys	Leu	Phe	Glu	
145					150					155					160	

AAT	ACC	AAG	ATT	AAC	CCT	AGG	GAT	ATT	GGT	GTG	TTG	GTT	GTG	AAT	TGT	528
Asn	Thr	Lys	Ile	Asn	Pro	Arg	Asp	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	
				165					170					175		

AGC	TTG	TTT	AAT	CCT	ACA	CCT	TCG	TTG	TCA	GCT	ATG	ATT	GTT	AAC	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			

TAT	AAG	CTT	AGA	GGG	AAT	GTT	AAG	AGT	TTT	AAC	CTG	GGG	GGC	ATT	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Ile		
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

AAG	CTT	AAG	TTA	TGG	TAT	CAC	TAC	CTG	ATT	TCT	CAC	CTT	TTT	AAG	CTC	48
Lys	Leu	Lys	Leu	Trp	Tyr	His	Tyr	Leu	Ile	Ser	His	Leu	Phe	Lys	Leu	
1				5					10					15		

TTG	TTG	GTT	CCT	TTA	ATG	GCG	GTT	CTG	TTC	ACG	AAT	GTC	TCC	CGG	TTA	96
Leu	Leu	Val	Pro	Leu	Met	Ala	Val	Leu	Phe	Thr	Asn	Val	Ser	Arg	Leu	
			20					25					30			

AGC	CTA	AAC	CAG	CTC	TGT	CTC	GAT	CTC	TCT	CTC	CAG	CTC	CAG	TTC	AAT	144
Ser	Leu	Asn	Gln	Leu	Cys	Leu	Asp	Leu	Ser	Leu	Gln	Leu	Gln	Phe	Asn	
		35					40					45				

CTC	GTC	GGA	TTC	ATC	TTC	TTC	ATT	ACC	GTC	TCC	ATT	TTC	GGA	TTC	ACA	192
Leu	Val	Gly	Phe	Ile	Phe	Phe	Ile	Thr	Val	Ser	Ile	Phe	Gly	Phe	Thr	
	50					55					60					

GTT	ATC	TTC	ATG	TCC	CGA	CCT	AGA	TCC	GTT	TAC	CTC	CTC	GAC	TAC	TCA	240
Val	Ile	Phe	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Leu	Asp	Tyr	Ser	
65					70				75						80	

TGT	TAC	CTC	CCG	CCG	TCG	AAT	CTC	AAA	GTT	AGC	TAC	CAG	ACA	TTC	ATG	288
Cys	Tyr	Leu	Pro	Pro	Ser	Asn	Leu	Lys	Val	Ser	Tyr	Gln	Thr	Phe	Met	
			85						90					95		
AAT	CAT	TCT	AAA	CTG	ATT	GAA	GAT	TTC	GAC	GAG	TCG	TCG	CTT	GAG	TTC	336
Asn	His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asp	Glu	Ser	Ser	Leu	Glu	Phe	
			100					105					110			
CAG	CGG	AAG	ATC	CTG	AAG	CGA	TCC	GGT	CTC	GGC	GAA	GAG	ACT	TAC	CTC	384
Gln	Arg	Lys	Ile	Leu	Lys	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	
		115					120					125				
CCG	GAA	TCT	ATC	CAC	TGC	ATC	CCG	CCG	CGT	CCG	ACT	ATG	GCG	GCG	GCG	432
Pro	Glu	Ser	Ile	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	
	130					135					140					
CGT	GAG	GAA	TCG	GAG	CAG	GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTC	TTC	480
Arg	Glu	Glu	Ser	Glu	Gln	Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	
145					150					155					160	
GAG	AAT	ACC	AAA	ATC	GAC	CCT	AGG	GAG	ATT	GGT	GTT	GTG	GTG	GTG	AAC	528
Glu	Asn	Thr	Lys	Ile	Asp	Pro	Arg	Glu	Ile	Gly	Val	Val	Val	Val	Asn	
				165					170					175		
TGC	AGC	TTG	TTT	AAC	CCG	ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTG	AAC	576
Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	
			180					185					190			
AAG	TAT	AAG	CTT	AGA	GGA	AAC	GTG	AAG	AGC	TTT	AAT	CTC	GGT	GGC	ATG	G 625
Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
G TTCATTGAT TTGTTTGAGA CTCTGTTGCA GAAATCTCCA C ATG GAT GAT GAA TCC 56
                                     Met Asp Asp Glu Ser
                                     1           5

GTT AAT GGA GGA TCC GTA CAG ATC CGG ACC CGA AAG TAC GTC AAG CTG 104
Val Asn Gly Gly Ser Val Gln Ile Arg Thr Arg Lys Tyr Val Lys Leu
          10          15          20

GGT TAT CAC TAC CTG ATT TCT CAC CTT TTT AAG CTC TTG TTG GTT CCT 152
Gly Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu Leu Leu Val Pro
          25          30          35

TTA ATG GCG GTT CTG TTC ACG AAT GTC TCC CGG TTA AGC CTA AAC CAG 200
Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu Ser Leu Asn Gln
          40          45          50

CTC TGT CTC GAT CTC TCT CTC CAG CTC CAG TTC AAT CTC GTC GGA TTC 248
Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn Leu Val Gly Phe
          55          60          65

ATC TTC TTC ATT ACC GCC TCC ATT TTC GGA TTC ACA GTT ATC TTC ATG 296
Ile Phe Phe Ile Thr Ala Ser Ile Phe Gly Phe Thr Val Ile Phe Met
          70          75          80          85

TCC CGA CCT AGA TCC GTT TAC CTC CTC GAC TAC TCA TGT TAC CTC CCG 344
Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro
          90          95          100

NCG GCG AAT CTC AAA GTT AGC TAC CAG ACA TTC ATG AAT CAT TCT AAA 392
Xxx Ala Asn Leu Lys Val Ser Tyr Gln Thr Phe Met Asn His Ser Lys
          105          110          115

CTG ATT GAA GAT TTC GAC GAG TCG TCG CTT GAG TTC CAG CGG AAG ATC 440
Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe Gln Arg Lys Ile
          120          125          130
```

CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC CCG GAA TCT ATC	488
Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Glu Ser Ile	
135 140 145	
CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG GCG CGT GAG GAA TCG	536
His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ser	
150 155 160 165	
GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC GAG AAT ACC AAA	584
Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys	
170 175 180	
ATC GAC CCT AGG GAG ATT GGT GTT GTG GTG GTG AAC TGC AGC TTG TTT	632
Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn Cys Ser Leu Phe	
185 190 195	
AAC CCG ACG CCT TCT TTA TCC GCC ATG ATT GTG AAC AAG TAT AAG CTT	680
Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu	
200 205 210	
AGA GGA AAC GTG AAG AGC TTT AAC CTC GGA GGA ATG GGA TGT AGG GCT	728
Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Arg Ala	
215 220 225	
GGT GTC ATC GCC GTT GAT CTC GCT AAT GAC ATT TTA CAG CTC CAT AGA	776
Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg	
230 235 240 245	
AAC ACA TTA GCT CTT GTG GTT AGC ACA GAG AAC ATC ACT CAG AAT TGG	824
Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp	
250 255 260	
TAC TTT GGT AAC AAC AAA GCA ATG TTG ATT CCT AAT TGC TTG TTT AGG	872
Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg	
265 270 275	
GTT GGT GGA TCC GCG GTT CTG CTT TCG AAC AAG CCT CGT GAT CGA AAA	920
Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys	
280 285 290	
CGA TCC AAG TAT AAA CTT GTT CAC ACG GTA CGG ACT CAT AAA GGA TCT	968
Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser	
295 300 305	

GAT	GAG	AAA	GCA	TTC	AAC	TGT	GTG	TAC	CAA	GAA	CAA	GAC	GAG	GAC	TTG	1016
Asp	Glu	Lys	Ala	Phe	Asn	Cys	Val	Tyr	Gln	Glu	Gln	Asp	Glu	Asp	Leu	
310					315					320					325	
AAA	ACC	GGA	GTT	TCT	TTG	TCT	AAA	GAC	CTA	ATG	TCT	ATA	GCT	GGA	GAA	1064
Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Leu	Met	Ser	Ile	Ala	Gly	Glu	
				330					335					340		
GCT	CTA	AAG	ACA	AAT	ATC	ACC	ACT	TTG	GGT	CCT	CTG	GTT	CTT	CCA	ATA	1112
Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Ile	
			345					350					355			
AGC	GAG	CAG	ATT	CTG	TTC	ATT	GCG	ACT	TTT	GTT	GCA	AAG	AGA	TTG	TTC	1160
Ser	Glu	Gln	Ile	Leu	Phe	Ile	Ala	Thr	Phe	Val	Ala	Lys	Arg	Leu	Phe	
		360					365					370				
AGT	GCC	AAG	AAG	AAG	AAG	AAG	AAG	CCT	TAC	ATA	CCG	GAT	TTC	AAG	CTT	1208
Ser	Ala	Lys	Lys	Lys	Lys	Lys	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	
	375					380					385					
GCC	TTT	GAT	CAT	TTC	TGT	ATT	CAC	GCA	GGA	GGT	AGA	GCC	GTG	ATC	GAT	1256
Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	
390					395					400					405	
GAA	CTA	GAG	AAG	AGT	TTA	AAG	CTA	TTG	CCA	AAA	CAT	GTG	GAG	GCT	TCT	1304
Glu	Leu	Glu	Lys	Ser	Leu	Lys	Leu	Leu	Pro	Lys	His	Val	Glu	Ala	Ser	
				410					415					420		
AGA	ATG	ACA	TTG	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCG	AGC	TCT	ATT	TGG	1352
Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	
			425					430					435			
TAT	GAA	TTA	GCT	TAC	ACA	GAA	GCT	AAA	GGA	AGA	ATG	AGA	AAA	GGG	AAT	1400
Tyr	Glu	Leu	Ala	Tyr	Thr	Glu	Ala	Lys	Gly	Arg	Met	Arg	Lys	Gly	Asn	
		440					445					450				
CGA	GTT	TGG	CAG	ATT	GCT	TTT	GGA	AGC	GGC	TTT	AAG	TGT	AAC	AGC	GCG	1448
Arg	Val	Trp	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	
	455					460					465					

GTT TGG GTG GCT CTT CGT GAT GTC GAG CCC TCG GTT AAC AAT CCT TGG 1496  
 Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp  
 470 475 480 485

GAA CAT TGC ATC CAT AGA TAT CCG GTT AAG ATC GAT CTC TGATTTTCAGC 1545  
 Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu  
 490 495

TTAACCGGTA AAATTGGTCT GTACATATAT TTACCACTGA GTAAAGACAT CAGTTAATGA 1605

TTTGTTGTGA CTCAATTGGG CTAAGTGTAT TATTATATGT GTTGTATATA ATAAAGGTAG 1665

AACGTAAATT TACTAAGAAA AAAAAAAAAA AAAAAAAAAA 1704

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CA ATG ACG TCT GTG AAC GTA AAA CTC CTT TAC CAT TAC GTC ATA ACC 47  
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr  
 1 5 10 15

AAC TTT TTC AAC CTC TGT TTC TTC CCA CTG ACG GGG ATC CTC GCC GGA 95  
 Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly  
 20 25 30

AAA GGC TCT CGT CTT ACC ACA AAC GAT CTC CAC CAC TTC TAT TCA TAT 143  
 Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr  
 35 40 45



CTC	CAA	CAC	AAN	CTT	ATA	ACC	TTA	ACC	CTA	CTC	TTT	GGC	TTC	ACC	GTT	191
Leu	Gln	His	Xxx	Leu	Ile	Thr	Leu	Thr	Leu	Leu	Phe	Gly	Phe	Thr	Val	
	50						55					60				
TTT	GGT	TCG	GTT	CTC	TAC	TTC	GTA	ANC	CGA	CCC	AAA	CCG	GTT	TAC	CTC	239
Phe	Gly	Ser	Val	Leu	Tyr	Phe	Val	Xxx	Arg	Pro	Lys	Pro	Val	Tyr	Leu	
	65					70					75					
GTT	GAC	TAC	TCC	TGC	TAC	CTT	CCA	CCA	CAA	CAT	CTT	AGC	GCT	GGT	ATC	287
Val	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Gln	His	Leu	Ser	Ala	Gly	Ile	
80					85					90					95	
TCT	AAG	ACC	ATG	GAA	ATC	TTT	TAT	CAA	ATA	AGA	AAA	TCT	GAT	CCT	TTA	335
Ser	Lys	Thr	Met	Glu	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ser	Asp	Pro	Leu	
				100					105					110		
CGA	AAC	GTG	GCA	TTA	GAT	GAT	TCG	TCT	TCT	CTT	GAT	TTC	TTG	AGA	AAG	383
Arg	Asn	Val	Ala	Leu	Asp	Asp	Ser	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
			115					120					125			
ATT	CAA	GAG	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACC	TAC	GGC	CCC	GAG	GGA	431
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Gly	Pro	Glu	Gly	
		130					135					140				
CTG	TTT	GAG	ATT	CCT	CCG	AGG	AAG	AAT	TTA	GCG	TCG	GCG	CGT	GAA	GAG	479
Leu	Phe	Glu	Ile	Pro	Pro	Arg	Lys	Asn	Leu	Ala	Ser	Ala	Arg	Glu	Glu	
	145					150					155					
ACG	GAG	CAA	GTA	ATC	AAC	GGT	GCG	CTA	AAA	AAT	CTA	TTC	GAG	AAC	AAC	527
Thr	Glu	Gln	Val	Ile	Asn	Gly	Ala	Leu	Lys	Asn	Leu	Phe	Glu	Asn	Asn	
160					165					170					175	
AAA	GTT	AAC	CCT	AAA	GAG	ATT	GGT	ATA	CTT	GTG	GTG	AAC	TCA	AGC	ATG	575
Lys	Val	Asn	Pro	Lys	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
				180					185					190		
TTT	AAT	CCG	ACT	CCT	TCG	TTA	TCC	GCG	ATG	GTA	GTT	AAT	ACT	TCC	AAG	623
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Ser	Lys	
			195					200					205			

CTC	CGA	AGC	AAC	ATC	AAA	AGC	TTT	AAT	CTT	GGA	GGA	ATG	GGT	TGC	AGT	671
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
		210					215					220				
GCT	GGT	GTT	ATC	GCC	ATT	GAT	CTA	GCT	AAA	GAC	TTG	TTG	CAT	GTT	CAT	719
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
	225					230					235					
AAA	AAC	ACA	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	CAA	AAC	767
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn	
240					245					250					255	
ATT	TAT	ACC	GGT	GAT	AAC	AGA	TCC	ATG	ATG	GTT	TCG	AAT	TGC	TTG	TTC	815
Ile	Tyr	Thr	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
				260					265					270		
CGT	GTC	GGT	GGG	GCA	GCG	ATT	CTG	CTC	TCC	AAC	AAG	CCG	GGG	GAT	CGA	863
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
			275					280					285			
AGA	CGG	TCC	AAG	TAC	AAG	CTA	GCT	CAC	ACG	GTT	CGA	ACG	CAT	ACC	GGA	911
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Ala	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290					295					300				
GCT	GAC	GAC	AAG	TCT	TTT	GGA	TGT	GTG	CGG	CAA	GAA	GAA	GAT	GAT	AGC	959
Ala	Asp	Asp	Lys	Ser	Phe	Gly	Cys	Val	Arg	Gln	Glu	Glu	Asp	Asp	Ser	
	305					310					315					
GGT	AAA	ACC	GGA	GTT	AGT	TTG	TCA	AAA	GAC	ATA	ACC	GTT	GTT	GCC	GGG	1007
Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Val	Val	Ala	Gly	
320					325					330					335	
ATA	ACG	GTT	CAG	AAA	AAC	ATA	ACA	ACA	TTG	GGT	CCG	TTG	GTT	CTT	CCT	1055
Ile	Thr	Val	Gln	Lys	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	
				340					345					350		
CTG	AGC	GAA	AAA	ATC	CTT	TTT	GTC	GTT	ACA	TTC	GTA	GCC	AAG	AAA	CTA	1103
Leu	Ser	Glu	Lys	Ile	Leu	Phe	Val	Val	Thr	Phe	Val	Ala	Lys	Lys	Leu	
			355					360					365			
TTA	AAA	GAT	AAG	ATC	AAA	CAC	TAT	TAC	GTG	CCG	GAT	TTC	AAA	CTT	GCA	1151
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
		370					375					380				

GTA	GAT	CAT	TTC	TGT	ATT	CAT	GCG	GGA	GGT	AGA	GCC	GTG	ATA	GAT	GTG	1199
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
	385					390					395					
TTA	GAG	AAG	AAC	TTA	GGG	CTA	TCG	CCG	ATA	GAT	GTG	GAG	GCA	TCA	AGA	1247
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
400					405					410					415	
TCA	ACA	TTA	CAT	AGA	TTT	GGG	AAT	ACA	TCG	TCT	AGT	TCA	ATT	TGG	TAT	1295
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
				420					425					430		
GAA	TTA	GCA	TAC	ATA	GAG	CCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	AAT	AAA	1343
Glu	Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
			435					440					445			
GCT	TGC	CAA	ATA	GCT	GGT	GGG	TCA	GGT	TTT	AAG	TGT	AAT	AGT	GCG	GTT	1391
Ala	Cys	Gln	Ile	Ala	Gly	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
		450					455					460				
TGG	GTC	GCT	TTA	CGC	AAT	GTC	GAG	GCT	TCA	GCT	AAT	AGT	CCT	TGG	GAA	1439
Trp	Val	Ala	Leu	Arg	Asn	Val	Glu	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Glu	
	465					470					475					
CAT	TGC	ATT	CAC	AAA	TAT	CCG	GTT	CAA	ATG	TAT	TCT	GGT	TCA	TCA	AAG	1487
His	Cys	Ile	His	Lys	Tyr	Pro	Val	Gln	Met	Tyr	Ser	Gly	Ser	Ser	Lys	
480					485					490					495	
TCA	GAG	ACT	CCT	GTC	CAA	AAC	GGT	CGG	TCC	TAATTTATGT	ATCTCAAATG					1537
Ser	Glu	Thr	Pro	Val	Gln	Asn	Gly	Arg	Ser							
				500												
ATGTTGTCCA CTTTCTCTTT TTTTTTTTCT TTTTITAGTT ATAATTTAAT GGTTACGATG																1597
TTTTGTCTAG GTCGTTATAA ATAAAGAATA CATGGGTGTT ACTAGTATAA AAAAAAAAAA																1657
AAAAAAA																1664

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTTCTTCTT	CCCCAACA	ATG	ACC	CAT	AAC	CAA	AAC	CAA	CCT	CAC	CGG	GCA	51			
		Met	Thr	His	Asn	Gln	Asn	Gln	Pro	His	Arg	Ala				
		1				5					10					
GTT	CCG	GTT	CAC	GTT	ACA	AAC	TCC	GAT	CAA	AAC	CAA	AAC	CAA	99		
Val	Pro	Val	His	Val	Thr	Asn	Ser	Asp	Gln	Asn	Gln	Asn	Gln			
			15					20					25			
AAC	AAT	CTC	CCA	AAT	TTT	CTC	TTA	TCT	GTT	CGG	CTC	AAA	TAT	GTA	147	
Asn	Asn	Leu	Pro	Asn	Phe	Leu	Leu	Ser	Val	Arg	Leu	Lys	Tyr	Val	Lys	
		30					35					40				
CTT	GGG	TAC	CAT	TAC	CTA	ATC	TCC	AAC	GGT	CTC	TAC	ATC	CTC	CTC	195	
Leu	Gly	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Gly	Leu	Tyr	Ile	Leu	Leu	Leu	
	45					50					55					
CCT	CTC	CTC	GGC	GGC	ACA	ATC	GTA	AAA	CTC	TCT	TCC	TTC	ACA	CTC	243	
Pro	Leu	Leu	Gly	Gly	Thr	Ile	Val	Lys	Leu	Ser	Ser	Phe	Thr	Leu	Asn	
60					65					70					75	
GAA	CTC	TCT	CTC	CTC	TAC	AAC	CAC	CTC	CGT	TTT	CAT	TTC	CTC	TCC	GCC	291
Glu	Leu	Ser	Leu	Leu	Tyr	Asn	His	Leu	Arg	Phe	His	Phe	Leu	Ser	Ala	
				80					85					90		
ACA	CTC	GCT	ACC	GGA	CTC	TTA	ATC	TCT	CTC	TCC	ACC	GCC	TAC	TTC	ACC	339
Thr	Leu	Ala	Thr	Gly	Leu	Leu	Ile	Ser	Leu	Ser	Thr	Ala	Tyr	Phe	Thr	
			95					100					105			
ACC	CGT	CCT	CGT	CAT	GTC	TTC	CTC	CTC	GAC	TTC	TCA	TGC	TAC	AAA	CCT	387
Thr	Arg	Pro	Arg	His	Val	Phe	Leu	Leu	Asp	Phe	Ser	Cys	Tyr	Lys	Pro	
		110					115					120				

GAC	CCT	TCC	TTA	ATA	TGC	ACT	CGT	GAA	ACA	TTC	ATG	GAC	CGA	TCT	CAA	435
Asp	Pro	Ser	Leu	Ile	Cys	Thr	Arg	Glu	Thr	Phe	Met	Asp	Arg	Ser	Gln	
	125					130					135					
CGT	GTA	GGT	ATC	TTC	ACA	GAA	GAC	AAC	CTC	GCT	TTT	CAA	CAA	AAG	ATC	483
Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	Gln	Lys	Ile	
140					145					150					155	
CTC	GAA	AGA	TCC	GGT	CTT	GGG	CAG	AAA	ACT	TAC	TTC	CCT	GAA	GCT	CTT	531
Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	Glu	Ala	Leu	
				160					165					170		
CTT	CGT	GTT	CCT	CCC	AAT	CCT	TGT	ATG	GAA	GAA	GCG	AGA	AAA	GAA	GCA	579
Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	Lys	Glu	Ala	
			175					180						185		
GAG	ACT	GTT	ATG	TTC	GGA	GCT	ATA	GAC	TCT	GTT	CTT	GAG	AAA	ACC	GGT	627
Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ser	Val	Leu	Glu	Lys	Thr	Gly	
		190					195					200				
GTG	AAA	CCT	AAA	GAT	ATC	GGA	ATC	CTT	GTC	GTG	AAT	TGT	AGT	TTG	TTT	675
Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	
	205					210					215					
AAT	CCG	ACG	CCG	TCA	CTT	TCC	GCC	ATG	ATT	GTG	AAT	AAG	TAT	AAG	CTT	723
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	
220					225					230					235	
AGA	GGA	AAC	ATT	TTG	AGC	TAT	AAT	CTC	GGT	GGA	ATG	GGT	TGT	AGT	GCT	771
Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
				240					245					250		
GGA	CTT	ATC	TCC	ATT	GAT	CTC	GCT	AAA	CAG	CTT	CTT	CAG	GTC	CAA	CCA	819
Gly	Leu	Ile	Ser	Ile	Asp	Leu	Ala	Lys	Gln	Leu	Leu	Gln	Val	Gln	Pro	
			255					260					265			
AAC	TCA	TAC	GCA	CTA	GTG	GTG	AGC	ACA	GAG	AAC	ATA	ACC	TTA	AAC	TGG	867
Asn	Ser	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Leu	Asn	Trp	
		270					275					280				
TAC	TTA	GGC	AAC	GAC	CGA	TCA	ATG	CTT	CTC	TCT	AAC	TGC	ATC	TTC	CGT	915
Tyr	Leu	Gly	Asn	Asp	Arg	Ser	Met	Leu	Leu	Ser	Asn	Cys	Ile	Phe	Arg	
	285					290					295					

ATG	GGA	GGA	GCC	GCC	GTA	CTT	CTC	TCA	AAC	CGT	TCC	TCC	GAT	CGC	ACC	963
Met	Gly	Gly	Ala	Ala	Val	Leu	Leu	Ser	Asn	Arg	Ser	Ser	Asp	Arg	Thr	
300					305					310					315	
CGT	TCA	AAA	TAT	CAG	CTC	ATC	CAC	CCC	GTC	CGT	ACC	CAC	AAA	GGA	GCC	1011
Arg	Ser	Lys	Tyr	Gln	Leu	Ile	His	Pro	Val	Arg	Thr	His	Lys	Gly	Ala	
				320					325					330		
AAC	GAC	AAC	GCA	TTT	GGC	TGC	GTT	TAC	CAA	CGA	GAA	GAC	AAC	AAC	GAA	1059
Asn	Asp	Asn	Ala	Phe	Gly	Cys	Val	Tyr	Gln	Arg	Glu	Asp	Asn	Asn	Glu	
			335					340					345			
GAA	GAA	ACC	GCC	AAA	ATC	GGA	GTC	TCA	CTC	TCT	AAA	AAC	CTA	ATG	GCA	1107
Glu	Glu	Thr	Ala	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asn	Leu	Met	Ala	
		350					355					360				
ATA	GCC	GGA	GAA	GCT	CTC	AAG	ACA	AAC	ATA	ACA	ACA	CTC	GGA	CCA	CTA	1155
Ile	Ala	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	
	365					370					375					
GTC	TTA	CCA	ATG	TCC	GAA	CAG	ATT	CTG	TTT	TTC	CCA	ACA	CTC	GTG	GCT	1203
Val	Leu	Pro	Met	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Pro	Thr	Leu	Val	Ala	
380					385					390					395	
CGA	AAA	ATC	TTC	AAA	GTC	AAG	AAA	ATA	AAG	CCT	TAC	ATA	CCC	GAT	TTC	1251
Arg	Lys	Ile	Phe	Lys	Val	Lys	Lys	Ile	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	
				400					405					410		
AAG	CTA	GCT	TTC	GAG	CAT	TTC	TGC	ATC	CAT	GCG	GGA	GGT	AGA	GCA	GTG	1299
Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	
			415					420					425			
CTT	GAT	GAG	ATA	GAG	AAG	AAT	TTG	GAT	TTA	TCA	GAG	TGG	CAT	ATG	GAA	1347
Leu	Asp	Glu	Ile	Glu	Lys	Asn	Leu	Asp	Leu	Ser	Glu	Trp	His	Met	Glu	
		430					435					440				
CCA	TCG	AGG	ATG	ACT	TTA	AAC	CGG	TTT	GGT	AAT	ACT	TCG	AGT	AGC	TCA	1395
Pro	Ser	Arg	Met	Thr	Leu	Asn	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	
	445					450					455					

CTT TGG TAT GAA CTT GCG TAT AGT GAA GCT AAA GGG AGG ATT AAG AGA 1443  
 Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg  
 460 465 470 475

GGA GAT AGG ACT TGC CAA ATT GCG TTT GGA TCG GGA TTT AAG TGT AAT 1491  
 Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn  
 480 485 490

AGT GCG GTT TGG AAA GCT TTG AGA ACC ATT GAT CCT ATT GAT GAG AAG 1539  
 Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys  
                   495                  500                  505

AAG AAT CCA TGG AGT GAT GAG ATT CAT GAG TTT CCA GTT TCT GTT CCT 1587  
 Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro  
                   510                  515                  520

AGG ATC ACT CCA GTT ACT TCT AAC TAGTGT TTTT TTTTGGGTC CAACTAGGGA 1641  
 Arg Ile Thr Pro Val Thr Ser Asn  
                   525                  530

TAATATTTGT TATGGTTTTG TTCTTACGTA CGTACTTTAA GTGATTTAGT CTAAAAATAA 1701

ATTGGTTTCA TAAAAA AAAAAAAAAA A 1732

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 :

AAG CTT AAA CTA GTA TAC CAT TAC TTG ATC TCC AAC GCC ATG TAT TTG 48  
 Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu  
   1                  5                  10                  15

TTA ATG GTG CCG CTT CTA GCA GTA GCC TTT GCT CAT CTC TCC ACG TTG 96  
 Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu  
                   20                  25                  30

ACG ATT CAA GAT CTG GTT CAT CTT TGG GAA CAG CTT AAG TTC AAT TTA 144  
 Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu  
                   35                  40                  45



CTG	TCA	GTA	ACT	CTC	TGC	TCG	AGC	CTT	ATG	GTG	TTT	TTA	GGG	ACT	CTG	192
Leu	Ser	Val	Thr	Leu	Cys	Ser	Ser	Leu	Met	Val	Phe	Leu	Gly	Thr	Leu	
	50					55					60					
TAT	TTC	ATG	AGC	CGA	CCG	ACG	AAG	ATT	TAC	TTG	GTG	GAT	TTC	TCT	TGT	240
Tyr	Phe	Met	Ser	Arg	Pro	Thr	Lys	Ile	Tyr	Leu	Val	Asp	Phe	Ser	Cys	
65					70					75					80	
TAC	AAG	CCG	GAA	AAA	GAG	CGT	ATA	TGC	ACG	AGA	GAG	ATT	TTC	TAT	GAG	288
Tyr	Lys	Pro	Glu	Lys	Glu	Arg	Ile	Cys	Thr	Arg	Glu	Ile	Phe	Tyr	Glu	
				85					90					95		
AGA	TCG	AAA	CTA	ACT	GGG	AAT	TTT	ACC	GAT	GAT	AAT	TTA	ACT	TTC	CAA	336
Arg	Ser	Lys	Leu	Thr	Gly	Asn	Phe	Thr	Asp	Asp	Asn	Leu	Thr	Phe	Gln	
			100					105					110			
AAG	AAA	ATT	ATC	GAA	AGA	TCT	GGA	TTA	GGT	CAG	AAC	ACG	TAC	TTA	CCT	384
Lys	Lys	Ile	Ile	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Asn	Thr	Tyr	Leu	Pro	
		115					120					125				
GAG	GCC	GTT	CTA	CGG	GTT	CCG	CCC	AAT	CCG	TGT	ATG	GCG	GAG	GCT	AGA	432
Glu	Ala	Val	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Ala	Glu	Ala	Arg	
	130					135					140					
AAG	GAG	GCT	GAG	ATG	GTT	ATG	TTC	GGT	GCG	ATC	GAT	GAA	TTG	TTG	GAG	480
Lys	Glu	Ala	Glu	Met	Val	Met	Phe	Gly	Ala	Ile	Asp	Glu	Leu	Leu	Glu	
145					150				155						160	
AAA	ACC	GGG	GTT	AAA	CCT	AAG	GAT	ATC	GGT	ATT	CTT	GTG	GTG	AAT	TGC	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165					170					175		
AGC	TTG	TTC	AAT	CCG	ACG	CCG	TCT	CTG	TCC	GCA	ATG	GTG	GTT	AAT	CGG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Arg	
			180					185					190			
TAC	AAG	CTT	AGA	GGG	AAT	ATC	ATA	AGT	TAT	AAC	CTT	GGC	GGG	ATG	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Ile	Ser	Tyr	Asn	Leu	Gly	Gly	Met		
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

Asn Ile Thr Thr Leu Gly  
5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

Ser Asn Cys Lys Phe Gly  
5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG 42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :  
CUACUACUAC UAGTCGACGG ATCCTATTTG GAAGCTTTGA CATTGTTTAG 50

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE: Xaa at position 3 = Leu or Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :  
Lys Leu Xaa Tyr His Tyr  
5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A

41

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Asn Leu Gly Gly Met Gly Cys  
5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNGGNATGG G

41

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) DESCRIPTION: synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT

40

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Gly Phe Lys Cys Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other  
 (A) DESCRIPTION: synthetic oligonucleotide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :  
 CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTRAANC C

41

(2) INFORMATION FOR SEQ ID NO: 39:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other  
 (A) DESCRIPTION: synthetic oligonucleotide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :  
 CUACUACUAC UASWRTTRCA YTTRAANCC

29